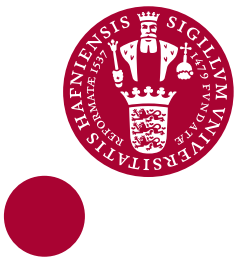

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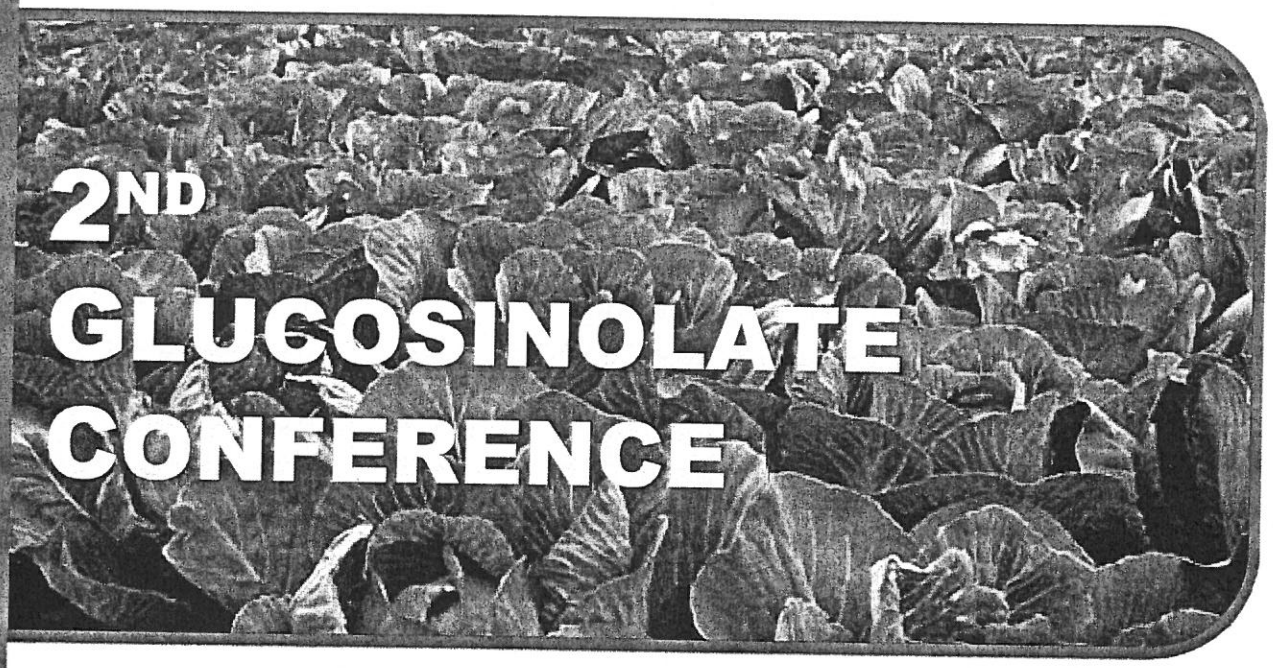

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Regulatory capabilities of the three R2 R3 MYB transcription factors regulating aliphatic glucosinolate biosynthesis

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Three members of the R2 R3 MYB transcription factor family, MYB28, MYB29 and MYB76 are the commonly defined regulators of the aliphatic glucosinolate biosynthesis. Each *MYB* gene has the capacity to increase aliphatic glucosinolates contents in leaves and seeds and induce gene expression of aliphatic biosynthetic genes within leaves when over-expressed. Leaves and seeds of single knockout mutants in *MYB29* and *MYB76* have reductions in only short-chained aliphatic glucosinolates whereas *MYB28* mutant has reductions in both short- and long-chained. This lead to a common regulatory model in which MYB28 is the dominant regulator, MYB29 plays a minor role and MYB76 is largely silent.

The first note of discord in this model arose via analysis showing that a double knockout in *MYB28* and *MYB29* was devoid of aliphatic glucosinolates, suggesting an interacting regulatory mechanism. Additional data suggesting the need for a revised model came from showing that a double knockout in *MYB28* and *MYB76* has an additive effect on foliar glucosinolate content in leaves thereby highlighting the importance of MYB76 *in planta*. Further, we have shown that MYB76 does not depend on MYB28 and MYB29 to induce aliphatic glucosinolates. Thus, we are working to better model the full regulatory network for aliphatic glucosinolates.

Finally, our recent transcriptional profiling of the knockouts revealed that glucosinolate levels in the plant are uncoupled from the level of transcription of aliphatic glucosinolate biosynthetic genes. Despite having a similar aliphatic glucosinolate decrease, the knockouts have different transcriptional profiles even when querying the glucosinolate genes. In summation, this new data suggests that the three MYBs have different regulatory functions that cooperatively interact to shape the plants glucosinolate profile.